

Appendix A

Gap Results SEQ ID NO: 1 vs. SEQ ID NO: 2

GAP of: SID 1 check: 418 from: 1 to: 476

WPDEF SVBV E3 Promoter fragment

to: SID 2 check: 1650 from: 1 to: 518

WPDEF SVBV E3 Promoter

Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	4760	Length:	518
Ratio:	10.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	5
.	=	1

SID 1 x SID 2

October 12, 2004 11:44 ..

```
1 .....aactatgctgatgacaagataattctaataagcaat 36
      |||
1 ggatccccagcttaactatgctgatgacaagataattctaataagcaat 50
      |||
37 tattcagaattaatcaaggagaaagaattaataactctttcagaatatga 86
      |||
51 tattcagaattaatcaaggagaaagaattaataactctttcagaatatga 100
      |||
87 agcccgctttacaagtggccagctagctatcactgaaaagacagcaagac 136
      |||
101 agcccgctttacaagtggccagctagctatcactgaaaagacagcaagac 150
      |||
137 aatggtgtctcgatgcaccagaaccacatctttgcagcagatgtgaagca 186
      |||
151 aatggtgtctcgatgcaccagaaccacatctttgcagcagatgtgaagca 200
      |||
187 gccagagtgggtccacaagacgcactcagaaaaggcatcttctaccgacac 236
      |||
201 gccagagtgggtccacaagacgcactcagaaaaggcatcttctaccgacac 250
      |||
237 agaaaaagacaaccacagctcatcatccaacatgtagactgtcgttatgc 286
      |||
251 agaaaaagacaaccacagctcatcatccaacatgtagactgtcgttatgc 300
      |||
287 gtcggctgaagataagactgacccagggccagcactaaagaagaataat 336
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|||||
301 gtcggctgaagataagactgaccccaggccagcactaaagaagaaataat 350
337 gcaagtggctcctagctccaacttttagctttaataattatgtttcattatta 386
|||||
351 gcaagtggctcctagctccaacttttagctttaataattatgtttcattatta 400
387 ttctctgcttttgcctctatatataaagagccttgatatttcatttgaaggc 436
|||||
401 ttctctgcttttgcctctatatataaagagccttgatatttcatttgaaggc 450
437 agaggcgaacacacacacagaacctccctgcttacaacc..... 476
|||||
451 agaggcgaacacacacacagaacctccctgcttacaaccggatcgggct 500
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Gap Results SEQ ID NO: 1 vs. SEQ ID NO: 3GAP of: SID 1 check: 418 from: 1 to: 476

WPDEF SVBV E3 Promoter fragment

to: SID 3 check: 303 from: 1 to: 651

WPDEF seSVBV promoter

1-108 of SVBV replaced by 92-362 of SBVB

Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	3971	Length:	654
Ratio:	8.342	Gaps:	1
Percent Similarity:	85.201	Percent Identity:	85.201

Match display thresholds for the alignment(s):

	-	IDENTITY
:	=	5
.	%	1

SID 1 x SID 3

October 12, 2004 11:45 ..

```
1 .....aactatgctgatgacaagataattcta 27
151 cagaaaaagacaaccacagctcatcatccaacatgtagactgtcgttatg 200
28 ataagcaatttattcagaattaatcaaggagaaagaattaataactctttc 77
201 cgtaggctgaagataagactgaccccaggccagcactaaagaagaataa 250
78 agaatatgaagcccgcctttacaagtggccagctagctatcactgaaaaga 127
251 tgcaagtggctcctagct...ccacttttagcgctagctatcactgaaaaga 297
128 cagcaagacaatggtgtctcgatgcaccagaaccacatctttgcagcaga 177
298 cagcaagacaatggtgtctcgatgcaccagaaccacatctttgcagcaga 347
178 tgtgaagcagccagagtgggtccacaagacgcactcagaaaaggcatcttc 227
348 tgtgaagcagccagagtgggtccacaagacgcactcagaaaaggcatcttc 397
228 taccgacacagaaaaagacaaccacagctcatcatccaacatgtagactg 277
398 taccgacacagaaaaagacaaccacagctcatcatccaacatgtagactg 447
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278 tcgttatgcgtcggtgaagataagactgacccagggccagcactaaaga 327
   |||
448 tcgttatgcgtcggtgaagataagactgacccagggccagcactaaaga 497
   |||
328 agaaataatgcaagtggctcctagctccactttagctttaaataattatgtt 377
   |||
498 agaaataatgcaagtggctcctagctccactttagctttaaataattatgtt 547
   |||
378 tcattattattctctgcttttgcctctctatataaaagagcttgatttttca 427
   |||
548 tcattattattctctgcttttgcctctctatataaaagagcttgatttttca 597
   |||
428 ttggaaggcagagggcgaacacacacacagaaacctccctgcttacaacc. 476
   |||
598 ttggaaggcagagggcgaacacacacacagaaacctccctgcttacaaccg 647
   .
   .
   .
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Gap Results SEQ ID NO: 1 vs. SEQ ID NO: 4

GAP of: SID 1 check: 418 from: 1 to: 476

WPDEF SVBV E3 Promoter fragment

to: SID 4 check: 7979 from: 1 to: 701

WPDEF 1eSVBV

1-108 of SVBV replaced by 92-404 of SVBV

Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000

Quality:	4049	Length:	704
Ratio:	8.506	Gaps:	2
Percent Similarity:	88.161	Percent Identity:	88.161

Match display thresholds for the alignment(s):

	-	IDENTITY
:	=	5
.	-	1

SID 1 x SID 4

October 12, 2004 11:46 ..

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1 .....aactatgctgatgacaagataattctaataagcaattatt 40
      | | | | | | | | | | | | | | | | | | | | |
201 gtcggctgaagataagactgacccagggccagcactaaagaagaataat 250
      | | | | | | | | | | | | | | | | | | | | |
41 cagaattaatcaaggagaa....agaattaataactctttcagaatatga 86
      | | | | | | | | | | | | | | | | | | | | |
251 gcaagtggctcctagctccacttttagctttaataattatgtttcattatta 300
      | | | | | | | | | | | | | | | | | | | | |
87 agcccgctttacaagtggccagctagctatcactgaaaagacagcaagac 136
      | | | | | | | | | | | | | | | | | | | | |
301 ttctctgctt...ttgctctcgctagctatcactgaaaagacagcaagac 347
      | | | | | | | | | | | | | | | | | | | | |
137 aatggtgtctcgatgcaccagaaccacatctttgcagcagatgtgaagca 186
      | | | | | | | | | | | | | | | | | | | | |
348 aatggtgtctcgatgcaccagaaccacatctttgcagcagatgtgaagca 397
      | | | | | | | | | | | | | | | | | | | | |
187 gccagagtgggtccacaagacgcactcagaaaaggcatctttctaccgacac 236
      | | | | | | | | | | | | | | | | | | | | |
398 gccagagtgggtccacaagacgcactcagaaaaggcatctttctaccgacac 447
      | | | | | | | | | | | | | | | | | | | | |
237 agaaaaagacaaccacagctcatcatccaacatgtagactgtcgttatgc 286
      | | | | | | | | | | | | | | | | | | | | |
448 agaaaaagacaaccacagctcatcatccaacatgtagactgtcgttatgc 497

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287 gtcggctgaagataagactgaccccaggccagcactaaagaagaataat 336
    |||
498 gtcggctgaagataagactgaccccaggccagcactaaagaagaataat 547
    |||
337 gcaagtggctcctagctccactttagctttaataattatgtttcattatta 386
    |||
548 gcaagtggctcctagctccactttagctttaataattatgtttcattatta 597
    |||
387 ttctctgcttttgctctctatatataagagcttgtattttcatttgaaggc 436
    |||
598 ttctctgcttttgctctctatatataagagcttgtattttcatttgaaggc 647
    |||
437 agaggcgaacacacacacagaacctccctgcttacaaacc..... 476
    |||
648 agaggcgaacacacacacagaacctccctgcttacaaaccggatcgggct 697
    |||
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Multiple Sequence Alignment: SEQ ID NO: 1-4

Symbol comparison table: pileupdna.cmp CompCheck: 6876

GapWeight: 5
GapLengthWeight: 1

SID_1_pileup_405724.txt MSF: 716 Type: N October 8, 2004 12:10
Check: 6538 ..

Name: SID_1	Len: 476	Check: 2120	Weight: 1.00
Name: SID_2	Len: 518	Check: 8412	Weight: 1.00
Name: SID_3	Len: 651	Check: 1160	Weight: 1.00
Name: SID_4	Len: 701	Check: 4846	Weight: 1.00

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      1                                     50
SID_1 ~~~~~
SID_2 ~~~~~
SID_3 ggatccgctt tacaagtggc cacctagcta tcaactgaaa gacagcaaga
SID_4 ~gatccgctt tacaagtggc cacctagcta tcaactgaaa gacagcaaga

      51                                     100
SID_1 ~~~~~
SID_2 ~~~~~
SID_3 caatggtgtc tcgatgcacc agaaccacat ctttgcagca gatgtgaagc
SID_4 caatggtgtc tcgatgcacc agaaccacat ctttgcagca gatgtgaagc

      101                                    150
SID_1 ~~~~~
SID_2 ~~~~~
SID_3 agccagagtg gtccacaaga cgcactcaga aaaggcatct tctaccgaca
SID_4 agccagagtg gtccacaaga cgcactcaga aaaggcatct tctaccgaca

      151                                    200
SID_1 ~~~~~
SID_2 ~~~~~
SID_3 cagaaaaaga caaccacagc tcatcatcca acatgtagac tgcgttatg
SID_4 cagaaaaaga caaccacagc tcatcatcca acatgtagac tgcgttatg

      201                                    250
SID_1 ~~~~~ ~aactatgct gatgacaaga taattctaata aagcaattat
SID_2 tccccagct taactatgct gatgacaaga taattctaata aagcaattat
SID_3 cgtcggctga agataagact gacccaggc cagcaactaa gaagaaataa
SID_4 cgtcggctga agataagact gacccaggc cagcaactaa gaagaaataa

      251                                    300
SID_1 tcagaattaa tcaaggagaa agaattaata actctttcag aatatgaagc
SID_2 tcagaattaa tcaaggagaa agaattaata actctttcag aatatgaagc
SID_3 tgcagtggt cctagctcca ctttag....
SID_4 tgcagtggt cctagctcca ctttagcttt aataattatg tttcattatt

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301                                     350
SID_1 ccgctttaca agtg.gccag ctagctatca ctgaaaagac agcaagacaa
SID_2 ccgctttaca agtg.gccag ctagctatca ctgaaaagac agcaagacaa
SID_3 .....cg ctagctatca ctgaaaagac agcaagacaa
SID_4 attctctgct ttgtctctcg ctagctatca ctgaaaagac agcaagacaa

351                                     400
SID_1 tgggtgtctcg atgcaccaga accacatctt tgcagcagat gtgaagcagc
SID_2 tgggtgtctcg atgcaccaga accacatctt tgcagcagat gtgaagcagc
SID_3 tgggtgtctcg atgcaccaga accacatctt tgcagcagat gtgaagcagc
SID_4 tgggtgtctcg atgcaccaga accacatctt tgcagcagat gtgaagcagc

401                                     450
SID_1 cagagtggtc cacaagacgc actcagaaaa ggcattcttct accgacacag
SID_2 cagagtggtc cacaagacgc actcagaaaa ggcattcttct accgacacag
SID_3 cagagtggtc cacaagacgc actcagaaaa ggcattcttct accgacacag
SID_4 cagagtggtc cacaagacgc actcagaaaa ggcattcttct accgacacag

451                                     500
SID_1 aaaaagacaa ccacagctca tcatccaaca tgtagactgt cgttatgcgt
SID_2 aaaaagacaa ccacagctca tcatccaaca tgtagactgt cgttatgcgt
SID_3 aaaaagacaa ccacagctca tcatccaaca tgtagactgt cgttatgcgt
SID_4 aaaaagacaa ccacagctca tcatccaaca tgtagactgt cgttatgcgt

501                                     550
SID_1 cggctgaaga taagaatgac cccaggccag cactaaagaa gaataatgc
SID_2 cggctgaaga taagaatgac cccaggccag cactaaagaa gaataatgc
SID_3 cggctgaaga taagaatgac cccaggccag cactaaagaa gaataatgc
SID_4 cggctgaaga taagaatgac cccaggccag cactaaagaa gaataatgc

551                                     600
SID_1 aagtggctct agctccactt tagctttaat aattatggtt cattattatt
SID_2 aagtggctct agctccactt tagctttaat aattatggtt cattattatt
SID_3 aagtggctct agctccactt tagctttaat aattatggtt cattattatt
SID_4 aagtggctct agctccactt tagctttaat aattatggtt cattattatt

601                                     650
SID_1 ctctgctttt gctctctata taaagagctt gtattttcat ttgaaggcag
SID_2 ctctgctttt gctctctata taaagagctt gtattttcat ttgaaggcag
SID_3 ctctgctttt gctctctata taaagagctt gtattttcat ttgaaggcag
SID_4 ctctgctttt gctctctata taaagagctt gtattttcat ttgaaggcag

651                                     700
SID_1 aggcgaacac acacacagaa cctccctgct tacaacccg~ ~~~~~
SID_2 aggcgaacac acacacagaa cctccctgct tacaacccg atcgggctgc
SID_3 aggcgaacac acacacagaa cctccctgct tacaacccg atc~~~~~
SID_4 aggcgaacac acacacagaa cctccctgct tacaacccg atcgggctgc

701                                     716
SID_1 ~~~~~
SID_2 aggtctctaa ccatgg
SID_3 ~~~~~
SID_4 ag~~~~~
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